SCORE Search Results Details for Application 10823203 and Search Result us-10-823-203a-3.rag.

This page gives you Search Results detail for the Application 10823203 and Search Result us-10-823-203a-3.rag.

start

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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: August 4, 2006, 00:45:41 ; Search time 196 Seconds
(without alignments)
256.601 Million cell updates/sec

Title: US-10-823-203A-3
Perfect score: 545
Sequence: 1 MSLKSDEVFAKIAKRLESID.....EVDGQVELIFLLEPFIASLK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	545	100.0	110	8	ADT61142	Adt61142 Yellow fe
2	161.5	29.6	115	4	ABB65491	Abb65491 Drosophil
3	144	26.4	107	4	ABB61449	Abb61449 Drosophil
4	129.5	23.8	547	7	ADD47206	Add47206 Rat Prote
5	128.5	23.6	547	5	ABB57301	Abb57301 Mouse isc
6	127.5	23.4	143	7	ADJ70149	Adj70149 Human hea
7	127.5	23.4	547	7	ADJ71194	Adj71194 Human hea
8	127.5	23.4	547	8	ABM80093	Abm80093 Tumour-as
9	127.5	23.4	547	9	AEA81487	Aea81487 Human ste
10	118.5	21.7	735	2	AAW16329	Aaw16329 Human hos
11	118.5	21.7	735	4	AAB70387	Aab70387 Human hos
12	118.5	21.7	736	4	AAB20185	Aab20185 Human mul
13	118.5	21.7	736	4	AAB20184	Aab20184 Human mul
14	118.5	21.7	736	5	ABG96550	Abg96550 Human sho
15	118.5	21.7	736	7	ADE61951	Ade61951 Human Pro
16	118.5	21.7	736	7	ADE61947	Ade61947 Human Pro
17	118.5	21.7	736	7	ADE60838	Ade60838 Human Pro
18	118.5	21.7	736	9	AED01665	Aed01665 Human sol
19	118.5	21.7	736	10	AEE61873	Aee61873 Human mul

20	118.5	21.7	752	8	ADR66395	Adr66395 Human pro
21	118.5	21.7	752	8	ADR66737	Adr66737 Human pro
22	113.5	20.8	734	10	AEE61871	Aee61871 Rat multi
23	113.5	20.8	735	7	ADE60836	Ade60836 Rat Prote
24	113.5	20.8	735	7	ADE61945	Ade61945 Rat Prote
25	113.5	20.8	735	7	ADE61949	Ade61949 Rat Prote
26	107.5	19.7	735	10	AEE61875	Aee61875 Mouse mul
27	104	19.1	740	4	AAU32847	Aau32847 Novel hum
28	100	18.3	436	8	ADN24158	Adn24158 Bacterial
29	96	17.6	172	5	ABG60202	Abg60202 Human DIT
30	95.5	17.5	544	4	ABB65056	Abb65056 Drosophil
31	92.5	17.0	211	6	ABO00589	Abo00589 Novel hum
32	90	16.5	412	4	ABB61661	Abb61661 Drosophil
33	83	15.2	203	5	ADK36946	Adk36946 Novel hum
34	83	15.2	203	6	ABO00851	Abo00851 Polypepti
35	83	15.2	278	4	AAU23020	Aau23020 Novel hum
36	83	15.2	278	4	ABB10251	Abb10251 Human cDN
37	83	15.2	278	4	AAU18466	Aau18466 Human end
38	83	15.2	278	5	ABP66838	Abp66838 Human pol
39	83	15.2	345	7	ADJ70022	Adj70022 Human hea
40	83	15.2	345	9	AEA81491	Aea81491 Human hyp
41	83	15.2	357	4	AAU18345	Aau18345 Human end
42	83	15.2	406	4	ABP37971	Abp37971 Human GS9
43	83	15.2	418	4	AAB84367	Aab84367 Amino aci
44	83	15.2	418	4	AAG81260	Aag81260 Human AFP
45	83	15.2	418	5	AAU76223	Aau76223 Human 216

ALIGNMENTS

RESULT 1
ADT61142
ID ADT61142 standard; protein; 110 AA.
XX
AC ADT61142;
XX
DT 13-JAN-2005 (first entry)
XX
DE Yellow fever mosquito sterol carrier protein-2 (AeSCP-2).
XX
KW sterol carrier protein-2; AeSCP-2; cholesterol transport;
KW yellow fever mosquito.
XX
OS Aedes aegypti.
XX
PN US2004211865-A1.
XX
PD 28-OCT-2004.
XX
PF 13-APR-2004; 2004US-00823203.
XX
PR 25-APR-2003; 2003US-0465648P.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Lan Q, Krebs KC;
XX
DR WPI; 2004-765537/75.
DR N-PSDB; ADT61140, ADT61141.
XX
PT Novel isolated and purified Aedes aegypti sterol carrier protein-2
PT polypeptide or its fragment capable of intracellular cholesterol
PT transport, useful for identifying agonist or antagonist of biological
PT activity of polypeptide.
XX
PS Claim 2; SEQ ID NO 3; 23pp; English.
XX
CC The invention relates to an isolated and purified Aedes aegypti sterol
CC carrier protein-2 (AeSCP-2) polypeptide. The polypeptide useful for
CC identifying whether a compound is an agonist or antagonist of AeSCP-2
CC biological activity. The polypeptide is useful for identifying compounds
CC which bind to or interact with the polypeptide or its fragments. The
CC polypeptide is capable of intracellular cholesterol transport in
CC mosquitoes. The present sequence represents the amino acid sequence of
CC the yellow fever mosquito sterol carrier protein-2 (AeSCP-2).
XX
SQ Sequence 110 AA;

  Query Match   100.0%; Score 545; DB 8; Length 110;
  Best Local Similarity   100.0%; Pred. No. 7.1e-54;
  Matches 110; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MSLKSDEVFAKIAKRLESIDPANRQVEHVYKFRITQGGKVVKNWVMDLKNVKLVESDDAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db          1 MSLKSDEVFAKIAKRLESIDPANRQVEHVYKFRITQGGKVVKNWVMDLKNVKLVESDDAA 60

Qy         61 EATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLEPFIASLK 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLEPFIASLK 110


RESULT 2
ABB65491
ID   ABB65491 standard; protein; 115 AA.
XX
AC   ABB65491;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 23265.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL09594.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Disclosure; SEQ ID NO 23265; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 115 AA;

  Query Match             29.6%;  Score 161.5;  DB 4;  Length 115;
  Best Local Similarity   34.9%;  Pred. No. 3.5e-10;
  Matches   38;  Conservative   19;  Mismatches   49;  Indels    3;  Gaps    1;

Qy          1 MSLKSDEVFAKIAKRLESIDPANRQVEHVYKFRITQGGKVVKNWVMDLKNVKLVESDD-- 58
              |||:|| || ||   |:  :   : |  |: ::||: ||| | | :| || |  |
Db          1 MSLQSDAVFQKIIDGLKENEAKAKAVNGVFLYKITKDGKVAKEWTLDCKNAKAYEGPAQG 60

Qy         59 -AAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLEPFI 106
                : |||: |: |  |  | |  : |  : |::: | : |   | | :
Db         61 IKVDTTLTVADEDMVDIALGKLNPQAAFMKGKLKIAGNIMLTQKLAPLL 109


RESULT 3
ABB61449
ID   ABB61449 standard; protein; 107 AA.
XX
AC   ABB61449;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 11139.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
```

PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE) PE CORP NY.
XX
PI   Venter JC, Adams M, Li PWD, Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL05552.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Disclosure; SEQ ID NO 11139; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 107 AA;

  Query Match   26.4%; Score 144; DB 4; Length 107;
  Best Local Similarity   31.4%; Pred. No. 3.1e-08;
  Matches   33; Conservative   25; Mismatches   41; Indels   6; Gaps   3;

```
Qy          3 LKSDEVFAKIAKRLESIDPANRQVEHVYKFRITQG-GKVVKNWVMDLKNVKLVESDDAAE 61
              :||||:  ||  :|:  ||| | | : ::|  |   | ::|:  :|:       |  : :
Db          1 MKSDEIIEKIRNKLKESDPARRTVVNTFQFNFTDADGNLIKSMALDIYE----GSATSVD 56

Qy         62 ATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELI-FLLEPF 105
              | :|: |:  : :||     :| : |:| ::||  | |  :|| |
Db         57 AQVTISDEDFYLVGTKQKTFQEVLQQEKAKIDGDEEAINKMLEKF 101
```

RESULT 4
ADD47206
ID   ADD47206 standard; protein; 547 AA.
XX
AC   ADD47206;
XX
DT   02-DEC-2004 (revised)
DT   29-JAN-2004 (first entry)
XX
DE   Rat Protein AAA41726, SEQ ID NO 12900.
XX
KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS   Rattus norvegicus.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAA41726.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.

XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 547 AA;

Query Match 23.8%; Score 129.5; DB 7; Length 547;
Best Local Similarity 30.5%; Pred. No. 1.1e-05;
Matches 32; Conservative 27; Mismatches 41; Indels 5; Gaps 3;

```
Qy          4 KSDEVFAKIAKRLESI-DPANRQVEHVYKFRITQG-GKVVKNWVMDLKNVK---LVESDD 58
              |:: :| :| |:||   :   :::  :: |::  | |     ||:|:|| |   | :||
Db        432 KANLIFKEIEKKLEEEGEEFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPDSDK 491

Qy         59 AAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLE 103
                |: |:|| |  : |: || :  : |  | |::: | : |   |:
Db        492 KADCTITMADSDLLALMTGKMNPQSAFFQGKLKIAGNMGLAMKLQ 536
```

RESULT 5
ABB57301
ID ABB57301 standard; protein; 547 AA.
XX
AC ABB57301;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related protein sequence SEQ ID NO:843.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP004192.
XX
PR 18-MAY-2000; 2000JP-00145977.
XX
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR WPI; 2002-034733/04.
DR N-PSDB; ABI99762.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
PS Claim 2; Page 2091-2093; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular

CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
SQ Sequence 547 AA;

Query Match 23.6%; Score 128.5; DB 5; Length 547;
Best Local Similarity 31.4%; Pred. No. 1.5e-05;
Matches 33; Conservative 25; Mismatches 42; Indels 5; Gaps 3;

```
Qy          4 KSDEVFAKIAKRLESI-DPANRQVEHVYKFRITQG-GKVVKNWVMDLKNVK---LVESDD 58
              |:: || :| |:||   :   :::  :: |::  | |     ||:|:|| |   |  ||
Db        432 KANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDK 491

Qy         59 AAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLE 103
               |: |:|| |  : |: || :  : |  | |::: | : |   |:
Db        492 KADCTITMADSDLLALMTGKMNPQSAFFQGKLKIAGNMGLAMKLQ 536
```

RESULT 6
ADJ70149
ID ADJ70149 standard; protein; 143 AA.
XX
AC ADJ70149;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID1955.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 1955; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,

CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 143 AA;

Query Match 23.4%; Score 127.5; DB 7; Length 143;
Best Local Similarity 31.4%; Pred. No. 3.4e-06;
Matches 33; Conservative 24; Mismatches 43; Indels 5; Gaps 3;

```
Qy        4 KSDEVFAKIAKRLESI-DPANRQVEHVYKFRITQG-GKVVKNWVMDLKNVK---LVESDD 58
            |:: || :| |:||   :   :::  :: |::  | |     ||:|:|| |   |  ||
Db       28 KANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDK 87

Qy       59 AAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLE 103
              |: |:|| |    |: || :  : |  | |::: | : |   |:
Db       88 KADCTITMADSDFLALMTGKMNPQSAFFQGKLKITGNMGLAMKLQ 132
```

RESULT 7
ADJ71194
ID ADJ71194 standard; protein; 547 AA.
XX
AC ADJ71194;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID3000.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 3000; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 547 AA;

Query Match 23.4%; Score 127.5; DB 7; Length 547;
Best Local Similarity 31.4%; Pred. No. 1.9e-05;
Matches 33; Conservative 24; Mismatches 43; Indels 5; Gaps 3;

```
Qy          4 KSDEVFAKIAKRLESI-DPANRQVEHVYKFRITQG-GKVVKNWVMDLKNVK---LVESDD 58
              |:: || :| |:||   :   :::  :: |::  | |     ||:|:|| |   |  ||
Db        432 KANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDK 491

Qy         59 AAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLE 103
               |: |:|| |    |: || :  : |  | |::: | : |   |:
Db        492 KADCTITMADSDFLALMTGKMNPQSAFFQGKLKITGNMGLAMKLQ 536


RESULT 8
ABM80093
ID   ABM80093 standard; protein; 547 AA.
XX
AC   ABM80093;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Tumour-associated antigenic target (TAT) polypeptide PRO60860, SEQ:236.
XX
KW   Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   chromosome identification; chromosome mapping; gene mapping;
KW   gene therapy; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004030615-A2.
XX
PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD,  Zhang Z,  Zhou Y;
XX
DR   WPI; 2004-347921/32.
DR   N-PSDB; ACN37386.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 12; SEQ ID NO 236; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT polypeptide of the invention
XX
SQ   Sequence 547 AA;

  Query Match             23.4%;  Score 127.5;  DB 8;  Length 547;
  Best Local Similarity   31.4%;  Pred. No. 1.9e-05;
  Matches   33;  Conservative   24;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          4 KSDEVFAKIAKRLESI-DPANRQVEHVYKFRITQG-GKVVKNWVMDLKNVK---LVESDD 58
              |:: || :| |:||   :   :::  :: |::  | |     ||:|:|| |   |  ||
Db        432 KANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDK 491

Qy         59 AAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLE 103
               |: |:|| |    |: || :  : |  | |::: | : |   |:
```

```
Db        492 KADCTITMADSDFLALMTGKMNPQSAFFQGKLKITGNMGLAMKLQ 536


RESULT 9
AEA81487
ID   AEA81487 standard; protein; 547 AA.
XX
AC   AEA81487;
XX
DT   08-SEP-2005  (first entry)
XX
DE   Human sterol carrier protein 2.
XX
KW   Anorectic; obesity; cachexia; anabolic; genetic marker; skeletal muscle;
KW   drug screening.
XX
OS   Homo sapiens.
XX
PN   EP1548131-A2.
XX
PD   29-JUN-2005.
XX
PF   15-DEC-2004; 2004EP-00029642.
XX
PR   22-DEC-2003; 2003EP-00104899.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (OSTE/) OSTENSON C.
XX
PI   Clerc RG,  Duchateau-Nguyen G,  Gardes C,  Mizrahi J,  Ostenson C;
XX
DR   WPI; 2005-460899/47.
DR   N-PSDB; AEA81479.
XX
PT   Screening compounds that reduce and/or prevent obesity, and/or treat
PT   cachexia, by contacting a cell expressing down-regulated or up-regulated
PT   genes in skeletal muscle in obesity.
XX
PS   Claim 13; SEQ ID NO 10; 239pp; English.
XX
CC   The invention relates to screening for compounds that reduce and/or
CC   prevent obesity comprising contacting a cell expressing any of 6 down-
CC   regulated or 2 up-regulated genes in skeletal muscle in obesity, and
CC   measuring the expression of the gene, or a polypeptide encoded by the
CC   gene, where a compound which up-regulates or down-regulates gene
CC   expression is a compound which causes an increase of expression of the
CC   gene or of the polypeptide encoded by the gene. Also included are
CC   screening for compounds that bind to a polypeptide with any of AEA81486-
CC   AEA81493 and AEA81521-AEA81547 (comprising contacting a compound with the
CC   polypeptide, and determining the ability of the compound to bind the
CC   polypeptide), a kit for screening for compounds that reduce and/or
CC   prevent obesity (comprising a polypeptide selected from any of AEA81486-
CC   AEA81493 and AEA81521-AEA81547), a compound identified by the method
CC   cited above and a pharmaceutical formulation for the modulation of body
CC   weight (comprising a compound that modulates the activity of a
CC   polypeptide selected from AEA81486-AEA81493 and AEA81521-AEA81547, mixed
CC   with a pharmaceutical carrier). The genes or encoded polypeptides are
CC   useful as a target for screening of compounds that reduce and/or prevent
CC   obesity. The compound is useful in the preparation of a medicament for
CC   the treatment of obesity and/or cachexia. The present sequence is a
CC   protein from a human gene that is down regulated in skeletal muscle in
CC   obesity.
XX
SQ   Sequence 547 AA;

  Query Match             23.4%;  Score 127.5;  DB 9;  Length 547;
  Best Local Similarity   31.4%;  Pred. No. 1.9e-05;
  Matches   33;  Conservative   24;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          4 KSDEVFAKIAKRLESI-DPANRQVEHVYKFRITQG-GKVVKNWVMDLKNVK---LVESDD 58
              |:: || :| |:||   :   :::  :: |::  | |     ||:|:|| |   |  ||
Db        432 KANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDK 491

Qy         59 AAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVELIFLLE 103
                |: |:|| |    |: || :  : |  | |::: | : |   |:
Db        492 KADCTITMADSDFLALMTGKMNPQSAFFQGKLKITGNMGLAMKLQ 536


RESULT 10
AAW16329
ID   AAW16329 standard; protein; 735 AA.
XX
AC   AAW16329;
XX
DT   17-AUG-1997  (first entry)
```

XX
DE Human host cell protein NS1I-1.
XX
KW NS1I-1; non-structural protein 1 interactor 1; host cell protein;
KW influenza virus; replication; antiviral; virucide.
XX
OS Homo sapiens.
XX
PN WO9712967-A1.
XX
PD 10-APR-1997.
XX
PF 06-OCT-1995; 95WO-US013044.
XX
PR 06-OCT-1995; 95WO-US013044.
XX
PA (MOUN) MOUNT SINAI MEDICAL CENT.
XX
PI Palese P, Oneill R;
XX
DR WPI; 1997-226211/20.
DR N-PSDB; AAT63340.
XX
PT New isolated DNA which encodes viral interacting proteins - used in
PT assays to isolate products for inhibiting viral protein binding which is
PT required for infection, replication, assembly or release.
XX
PS Disclosure; Fig 12A-C; 98pp; English.
XX
CC Non-structural protein 1 interactor 1 (NS1I-1) (AAW16329) is a human host
CC cell protein which interacts with influenza virus protein NS1. It was
CC identified using a yeast interactive trap system. Its amino acid sequence
CC was deduced from ND1I-1 cDNA (AAT63340). Another host cell protein, NPI-1
CC (AAW63327), has also been identified. These host cell proteins can be
CC used in assays to identify cpds. that interfere with the specific
CC interaction between the viral and host cell proteins. Such cpds. can be
CC used to treat viral infection
XX
SQ Sequence 735 AA;

  Query Match   21.7%; Score 118.5; DB 2; Length 735;
  Best Local Similarity   28.7%; Pred. No. 0.0003;
  Matches   29; Conservative   25; Mismatches   42; Indels   5; Gaps   2;

Qy   3 LKSDEVFAKIAKRLESIDP-ANRQVEHVYKFRITQGGKVVKNWVMDLKN----VKLVESD 57
              |:| || :| :||: | | ::| |::: ||:|| : | :|||: | :
Db   621 LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAK 680

Qy   58 DAAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVEL 98
               ||: |: : |:   : | | ::| ::: | : |
Db   681 GAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIML 721

RESULT 11
AAB70387
ID AAB70387 standard; protein; 735 AA.
XX
AC AAB70387;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human host cell protein NP1I-1 protein sequence SEQ ID NO:13.
XX
KW Identification; antiviral; viral protein; viral replication; NP;
KW viral infection; nucleoprotein.
XX
OS Homo sapiens.
XX
PN WO200111335-A2.
XX
PD 15-FEB-2001.
XX
PF 11-AUG-2000; 2000WO-US022257.
XX
PR 11-AUG-1999; 99US-0148263P.
XX
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
PI O'neill R, Harty R, Palese PM;
XX
DR WPI; 2001-168816/17.
DR N-PSDB; AAF59400.
XX
PT Identifying a substance that inhibits the interaction between a viral
PT protein and a host cell protein, useful for the discovery of new

PT antiviral compounds.
XX
PS Example; Fig 12; 147pp; English.
XX
CC The present invention describes a method (M1) for identifying a substance
CC that inhibits the interaction of a viral protein (VP) with a host cell
CC protein (HP). The method comprises: (a) contacting HP with VP in the
CC presence of a test substance; and (b) detecting complex formation, where
CC the ability of the test substance to inhibit HP/VP interaction is
CC indicated by a decrease in complex formation. The antiviral compounds
CC that inhibit the interaction between a host protein (NS1-BP or NPI-1) and
CC a viral protein (NS1) are useful for treating or inhibiting viral
CC infection, preferably influenza and rhabdovirus infection, in humans.
CC Antiviral compounds include peptides and antibodies. In particular
CC compositions comprising a polypeptide containing an amino acid sequence
CC corresponding to the NP-NLS domain of the influenza virus NP protein,
CC which inhibits the specific interaction of the NPI-1 protein with the
CC influenza virus NP protein are useful for treating or inhibiting
CC influenza viral infection in humans. The present sequence represents a
CC human host cell protein designated NP1I-1, which is used in an example
CC from the present invention
XX
SQ Sequence 735 AA;

Query Match 21.7%; Score 118.5; DB 4; Length 735;
Best Local Similarity 28.7%; Pred. No. 0.0003;
Matches 29; Conservative 25; Mismatches 42; Indels 5; Gaps 2;

```
Qy          3 LKSDEVFAKIAKRLESIDP-ANRQVEHVYKFRITQGGKVVKNWVMDLKN----VKLVESD 57
              |:|  || :| :||: | |   ::|  |::: ||:|| :   | :|||:    |    :
Db        621 LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAK 680

Qy         58 DAAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVEL 98
               ||: |: : |:    :  | |  ::|    :::  | : |
Db        681 GAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIML 721
```

RESULT 12
AAB20185
ID AAB20185 standard; protein; 736 AA.
XX
AC AAB20185;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human multifunctional enzyme type 2 (MFE-2) mutant G16S.
XX
KW 2-Enoyl-CoA hydratase 2/(3R)-hydroxyacyl-CoA dehydrogenase; human;
KW multifunctional enzyme 2; MFE-2; 17-beta-hydroxysteroid dehydrogenase 4;
KW (3R)-hydroxyacyl-CoA ester; polyhydroxyalkanoate;
KW poly-beta-hydroxybutyrate; biodegradable plastic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200109364-A1.
XX
PD 08-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-FI000663.
XX
PR 03-AUG-1999; 99FI-00001667.
XX
PA (OULU-) OULUN YLIOPISTO.
XX
PI Hiltunen K, Glumoff T;
XX
DR WPI; 2001-191458/19.
XX
PT Novel modified gene encoding a multifunctional 2-enoyl-CoA hydratase
PT 2/(3R)-hydroxyacyl CoA dehydrogenase enzyme type 2 protein used to
PT control the production of polyhydroxyalkanoates (PHAs).
XX
PS Disclosure; Fig 11; 74pp; English.
XX
CC The present sequence is that of a human mutated multifunctional 2-enoyl-
CC CoA hydratase 2/(3R)-hydroxyacyl CoA dehydrogenase enzyme type 2 protein
CC (MFE-2) or 17-beta-hydroxysteroid dehydrogenase 4 protein in which the
CC native Gly-16 residue is replaced by Ser. According to the present
CC invention it is possible to alter the substrate specificity of MFE-2 and
CC thereby control the chain lengths of (3R)-hydroxyacyl-CoA intermediates
CC in the cellular (3R)-hydroxyacyl pool. Polyhydroxyalkanoate-synthetase
CC present in a production host uses the (3R)-hydroxyacyl-CoA intermediates
CC of desired chain lengths to synthesise polyhydroxyalkanoates (PHAs) with
CC desired chain lengths and properties. Mutation of human MFE-2 Gly-16 to

CC Ser results in accumulation (3R)-hydroxyacyl CoA esters of C8-C18 chain
CC length. This mutation is observed in human MFE-2 deficiency. The products
CC can be used in the production of biodegradable plastics such as poly-beta
CC -hydroxybutyrate. Monomeric 3-hydroxyacids with specific chain lengths
CC can be used as reagents in biomedical research. Fewer purification steps
CC are needed and no laborious or costly organic synthesis is required
XX
SQ Sequence 736 AA;

Query Match 21.7%; Score 118.5; DB 4; Length 736;
Best Local Similarity 28.7%; Pred. No. 0.0003;
Matches 29; Conservative 25; Mismatches 42; Indels 5; Gaps 2;

Qy 3 LKSDEVFAKIAKRLESIDP-ANRQVEHVYKFRITQGGKVVKNWVMDLKN----VKLVESD 57
Db 622 LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAK 681

Qy 58 DAAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVEL 98
Db 682 GAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIML 722

RESULT 13
AAB20184
ID AAB20184 standard; protein; 736 AA.
XX
AC AAB20184;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human multifunctional enzyme type 2 (MFE-2).
XX
KW 2-Enoyl-CoA hydratase 2/(3R)-hydroxyacyl-CoA dehydrogenase; human;
KW multifunctional enzyme 2; MFE-2; 17-beta-hydroxysteroid dehydrogenase 4;
KW (3R)-hydroxyacyl-CoA ester; polyhydroxyalkanoate;
KW poly-beta-hydroxybutyrate; biodegradable plastic.
XX
OS Homo sapiens.
XX
PN WO200109364-A1.
XX
PD 08-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-FI000663.
XX
PR 03-AUG-1999; 99FI-00001667.
XX
PA (OULU-) OULUN YLIOPISTO.
XX
PI Hiltunen K, Glumoff T;
XX
DR WPI; 2001-191458/19.
XX
PT Novel modified gene encoding a multifunctional 2-enoyl-CoA hydratase
PT 2/(3R)-hydroxyacyl CoA dehydrogenase enzyme type 2 protein used to
PT control the production of polyhydroxyalkanoates (PHAs).
XX
PS Disclosure; Fig 10; 74pp; English.
XX
CC The present sequence is that of human multifunctional 2-enoyl-CoA
CC hydratase 2/(3R)-hydroxyacyl CoA dehydrogenase enzyme type 2 protein (MFE
CC -2) or 17-beta-hydroxysteroid dehydrogenase 4. According to the present
CC invention it is possible to alter the substrate specificity of yeast or
CC mammalian MFE-2 and thereby to control the chain lengths of (3R)-
CC hydroxyacyl-CoA intermediates in the cellular (3R)-hydroxyacyl pool.
CC Polyhydroxyalkanoate-synthetase present in a production host uses the
CC (3R)-hydroxyacyl-CoA intermediates of desired chain lengths to synthesise
CC polyhydroxyalkanoates (PHAs) with desired chain lengths and properties.
CC Mutation of human MFE-2 Gly-16 to Ser results in accumulation (3R)-
CC hydroxyacyl CoA esters of C8-C18 chain length. This mutation is observed
CC on human MFE-2 deficiency. The products can be used in the production of
CC biodegradable plastics such as poly-beta-hydroxybutyrate. Monomeric 3-
CC hydroxyacids with specific chain lengths can be used as reagents in
CC biomedical research. Fewer purification steps are needed and no laborious
CC or costly organic synthesis is required
XX
SQ Sequence 736 AA;

Query Match 21.7%; Score 118.5; DB 4; Length 736;
Best Local Similarity 28.7%; Pred. No. 0.0003;
Matches 29; Conservative 25; Mismatches 42; Indels 5; Gaps 2;

Qy 3 LKSDEVFAKIAKRLESIDP-ANRQVEHVYKFRITQGGKVVKNWVMDLKN----VKLVESD 57
Db 622 LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAK 681

```
Qy          58 DAAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVEL 98
               ||: |: : |:    :  | |  ::|    :::  | : |
Db         682 GAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIML 722


RESULT 14
ABG96550
ID   ABG96550 standard; protein; 736 AA.
XX
AC   ABG96550;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human short chain dehydrogenase family member 17beta-HSD #3.
XX
KW   Short chain dehydrogenase; SDR; human; antimicotica; pesticide;
KW   herbicide; DHPR deficiency; phenylketonuria; galactosaemia III;
KW   dienoyl CoA reductase deficiency; adrenal hyperplasia; ovarian cancer;
KW   adrenogenital syndrome; mineralcorticoid excess syndrome; breast cancer;
KW   male psuedohermaphroditism; Zellweger syndrome; Down's syndrome;
KW   polycystic kidney disease; Alzheimer's disease; retinitis pigmentosa;
KW   retinitis punctata albescens; arterial hypertension; follicular lymphoma;
KW   hepatocarcinogenesis; fungicide; antibiotic.
XX
OS   Homo sapiens.
XX
PN   WO200212544-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-EP009140.
XX
PR   07-AUG-2000; 2000US-0223436P.
XX
PA   (BION-) BIONETWORKS GMBH.
XX
PI   Wilckens T;
XX
DR   WPI; 2002-241770/29.
XX
PT   Identifying or verifying members of the short chain dehydrogenase (SDR)
PT   family, useful for novel drug development (e.g. for the development of
PT   antimicotica, pesticides or herbicides), by employing an algorithm using
PT   core SDR motifs.
XX
PS   Disclosure; Fig 4; 168pp; English.
XX
CC   The invention relates to identifying or verifying members of the short
CC   chain dehydrogenase (SDR) family comprises employing an algorithm using
CC   core SDR motifs (MT1-MT4 and MV1, MV2 given in the specification) for
CC   searching members of the SDR family. Also included are a member of the
CC   SDR family identified with the method above, a method for providing
CC   modulators for members of the SDR family, a method for evaluation of lead
CC   -candidates for possible modulators of a member of the SDR family and a
CC   method for detecting clinically relevant polymorphisms or single
CC   nucleotide polymorphisms. The method is useful for screening SDR
CC   sequences and modulators of the SDR family. The method is especially
CC   useful as a platform for novel drug development. The SDRs can serve for
CC   the development of e.g. antimicotica, pesticides or herbicides. The
CC   modulators may be especially useful for the prophylaxis, treatment or/and
CC   diagnosis of diseases (e.g. DHPR deficiency, phenylketonuria, dienoyl CoA
CC   reductase deficiency, galactosaemia III, adrenal hyperplasia,
CC   adrenogenital syndrome, mineralcorticoid excess syndrome, ovarian cancer,
CC   breast cancer, male psuedohermaphroditism, Zellweger syndrome, polycystic
CC   kidney disease, Alzheimer's disease, retinitis punctata albescens,
CC   retinitis pigmentosa, Down's syndrome, arterial hypertension, follicular
CC   lymphoma and hepatocarcinogenesis) particularly as a fungicide or
CC   antibiotic. The present sequence is one of 39 human SDR family members
CC   identified by the method of the invention
XX
SQ   Sequence 736 AA;

  Query Match             21.7%;  Score 118.5;  DB 5;  Length 736;
  Best Local Similarity   28.7%;  Pred. No. 0.0003;
  Matches   29;  Conservative   25;  Mismatches   42;  Indels    5;  Gaps    2;

Qy           3 LKSDEVFAKIAKRLESIDP-ANRQVEHVYKFRITQGGKVVKNWVMDLKN----VKLVESD 57
               |:|  || :| :||: | |   ::|  |::: ||:|| :   | :|||:    |    :
Db         622 LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAK 681

Qy          58 DAAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVEL 98
               ||: |: : |:    :  | |  ::|    :::  | : |
Db         682 GAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIML 722
```

RESULT 15
ADE61951
ID   ADE61951 standard; protein; 736 AA.
XX
AC   ADE61951;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Human Protein P51659, SEQ ID NO 7880.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P51659.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 736 AA;

  Query Match   21.7%; Score 118.5; DB 7; Length 736;
  Best Local Similarity   28.7%; Pred. No. 0.0003;
  Matches   29; Conservative   25; Mismatches   42; Indels   5; Gaps   2;

Qy   3 LKSDEVFAKIAKRLESIDP-ANRQVEHVYKFRITQGGKVVKNWVMDLKN----VKLVESD 57
              |:| || :| :||: | | ::| |::: ||:|| : | :|||: | :
Db   622 LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAK 681

Qy   58 DAAEATLTMEDDIMFAIGTGALPAKEAMAQDKMEVDGQVEL 98
                ||: |: : |:   : | | ::| ::: | : |
Db   682 GAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIML 722

Search completed: August 4, 2006, 00:49:26
Job time : 200 secs